



# 8

# SEQUENCE LISTING

<110> Gish, Kurt  
Mack, David H.  
Wilson, Keith E.  
Eos Biotechnology, Inc.

<120> Methods of Diagnosis of Colorectal Cancer, Compositions  
and Methods of Screening for Colorectal Cancer  
Modulators

<130> 018501-003100US

<140> US 09/930,020

<141> 2001-08-14

<150> US 09/663,733

<151> 2000-09-15

<160> 3

<170> PatentIn Ver. 2.1

<210> 1

<211> 3375

<212> DNA

<213> Homo sapiens

<220>

<223> CBF9

<220>

<221> CDS

<222> (328)..(2751)

<223> CBF9

<400> 1

```
gacagtgttc gcggtctgcac cgctcggagg ctgggtgacc cgcgtagaag tgaagtactt 60
ttttatttgc agacctgggc cgatgccgct ttaaaaaacg cgaggggctc tatgcacctc 120
cctggcggtg gttcctccga cctcagccgg gtcgggtcgt gccgccctct cccaggagag 180
acaaacaggt gtccacgtg gcagccgcgc cccgggcgcc cctcctgtga tcccgtagcg 240
ccccctggcc cgagccgcgc cgggtctgt gagtagagcc gcccgggcac cagcgctgg 300
tcgcccgtct ccttcctgta tatcaacatg cccctttcc tgttgctgga ggccgtctgt 360
gttttcctgt tttccagagt gcccctctct ctcctctctc aggaagtcca tgtaagcaaa 420
gaaaccatcg ggaagatttc agctgccagc aaaatgatgt ggtgctcggc tgcagtggac 480
atcatgtttc tgtagatgg gtctaacagc gtcgggaaag ggagctttga aaggtccaag 540
cactttgcca tcacagtctg tgacggtctg gacatcagcc ccgagagggg cagagtggga 600
gcattccagt tcagttccac tctcatctg gaattccctc tggattcatt ttcaacccaa 660
caggaagtga aggcaagaat caagaggatg gttttcaaag gagggcgcac ggagacggaa 720
cttgctctga aataccttct gcacagaggg ttgcctggag gcagaaatgc tctgtgccc 780
cagatcctca tcacgtcac tgatgggaag tcccaggggg atgtggcact gccatccaag 840
cagctgaagg aaaggggtgt cactgtgttt gctgtggggg tcaggtttcc caggtgggag 900
gagctgcatg cactggccag cgagcctaga gggcagcacg tgctgttggc tgagcaggtg 960
gaggatgcc aacaggcct cttcagcacc ctcagcagct cggccatctg ctccagcgcc 1020
acgccagact gcagggtcga ggctcaccct tgtgagcaca ggacgctgga gatggtccgg 1080
gagttcgtg gcaatgcccc atgctggaga ggatcgcggc ggacccttgc ggtgctggct 1140
gcacactgtc ccttctacag ctggaagaga gtgttcctaa cccaccctgc cacctgtac 1200
aggaccacct gccaggccc ctgtgactcg cagccctgcc agaattggagg cacatgtgtt 1260
ccagaaggac tggacggcta ccagtgcctc tgcccgtgg cctttggagg ggaggctaac 1320
tgtgccctga agctgagcct ggaatgcagg gtcgacctcc tcttctgtct ggacagctct 1380
gcgggcacca ctctggacgg cttcctgcgg gccaaagtct tcgtgaagcg gtttgtgcgg 1440
```

```

gccgtgctga gcgaggactc tcggggccga gtgggtgtgg ccacatacag cagggagctg 1500
ctgggtggcgg tgccctgtggg ggagtagcag gatgtgcctg acctggtctg gagcctcgat 1560
ggcattccct tccgtgggtg ccccaacctg acgggcagtg ccttgccgga ggccgcagag 1620
cgtggcttcg ggagcgcac caggacaggc caggaccggc cacgtagagt ggtggttttg 1680
ctcactgagt cacactccga ggatgaggtt gcgggcccag cgcgtcacgc aagggcgcga 1740
gagctgctcc tgctgggtgt aggcagttag gccgtgcggg cagagctgga ggagatcaca 1800
ggcagcccaa agcatgtgat ggtctactcg gatcctcagg atctgttcaa ccaaatccct 1860
gagctgcagg ggaagctgtg cagccggcag cggccagggt gccggacaca agccctggac 1920
ctcgtcttca tgttggaacac ctctgcctca gtaggggccc agaattttgc tcagatgcag 1980
agctttgtga gaagctgtgc cctccagttt gaggtgaacc ctgacgtgac acaggtcggc 2040
ctgggtgggtg atggcagcca ggtgcagact gccttcgggc tggacaccaa acccaccggg 2100
gctgcgatgc tgcggggccat tagccaggcc ccctacctag gtgggtgtgg ctcagccggc 2160
accgccctgc tgcacatctc tgacaaagtg atgaccgtcc agaggggtgc ccggcctggt 2220
gtccccaag ctgtggtggt gctcacaggc gggagaggcg cagaggatgc agccgttctt 2280
gcccagaagc tgaggaacaa tggcatctct gtcttggtcg tggcgtggg gcctgtccta 2340
agtgagggtc tgcggagggt tgcaggctcc cgggattccc tgatccacgt gccagcttac 2400
gccgacctgc ggtaccacca ggacgtgctc attgagtggc tgtgtggaga agccaagcag 2460
ccagtcaacc tctgcaaacc cagccctgct atgaatgagg gcagctgctt cctgcagaat 2520
gggagctacc gctgcaagtg tcgggatggc tgggagggcc cccactgcca gaaccgtgag 2580
tggagctctt gctctgtatg tgtgagccag ggatggattc ttgagacgcc cctgaggcac 2640
atggctcccg tgcaggaggg cagcagccgt acccctccca gcaactacag agaaggcctg 2700
ggcactgaaa tgggtgctac cttctggaat gtctgtgccc caggtcctta gaatgtctgc 2760
ttcccgccgt ggccaggacc actattctca ctgagggagg aggatgtccc aactgcagcc 2820
atgctgctta gagacaagaa agcagctgat gtcaccacaa aacgatgttg ttgaaaagtt 2880
ttgatgtgta agtaaatacc cactttctgt acctgtgtgt ccttggtgag gctatgtcat 2940
ctgccacctt tcccttgagg ataaacaagg ggtcctgaag acttaaattt agcggcctga 3000
cgttcctttg cacacaatca atgctcgcca gaatgttgtt gacacagtaa tgcccagcag 3060
aggcctttac tagagcatcc tttggacggc gaaggccacg gcctttcaag atggaaagca 3120
gcagcttttc cacttcccca gagacattct ggatgcattt gcattgagtc tgaaaggggg 3180
cttgaggggac gtttgtgact tcttggcgac tgccctttgt gtgtggaaga gacttggaaa 3240
ggctcagac tgaatgtgac caattaacca gcttggttga tgatggggga ggggctgagt 3300
tgtgcatggg ccaggtctg gagggccacg taaaatcggt ctgagtcgtg agcagtgtcc 3360
accttgaagg tcttc

```

<210> 2  
 <211> 807  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> CBF9

<400> 2  
 Met Pro Pro Phe Leu Leu Leu Glu Ala Val Cys Val Phe Leu Phe Ser  
 1 5 10 15  
 Arg Val Pro Pro Ser Leu Pro Leu Gln Glu Val His Val Ser Lys Glu  
 20 25 30  
 Thr Ile Gly Lys Ile Ser Ala Ala Ser Lys Met Met Trp Cys Ser Ala  
 35 40 45  
 Ala Val Asp Ile Met Phe Leu Leu Asp Gly Ser Asn Ser Val Gly Lys  
 50 55 60  
 Gly Ser Phe Glu Arg Ser Lys His Phe Ala Ile Thr Val Cys Asp Gly  
 65 70 75 80  
 Leu Asp Ile Ser Pro Glu Arg Val Arg Val Gly Ala Phe Gln Phe Ser  
 85 90 95  
 Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Gln Gln  
 100 105 110  
 Glu Val Lys Ala Arg Ile Lys Arg Met Val Phe Lys Gly Gly Arg Thr  
 115 120 125

Glu	Thr	Glu	Leu	Ala	Leu	Lys	Tyr	Leu	Leu	His	Arg	Gly	Leu	Pro	Gly
130						135					140				
Gly	Arg	Asn	Ala	Ser	Val	Pro	Gln	Ile	Leu	Ile	Ile	Val	Thr	Asp	Gly
145					150					155					160
Lys	Ser	Gln	Gly	Asp	Val	Ala	Leu	Pro	Ser	Lys	Gln	Leu	Lys	Glu	Arg
				165					170					175	
Gly	Val	Thr	Val	Phe	Ala	Val	Gly	Val	Arg	Phe	Pro	Arg	Trp	Glu	Glu
			180					185					190		
Leu	His	Ala	Leu	Ala	Ser	Glu	Pro	Arg	Gly	Gln	His	Val	Leu	Leu	Ala
		195					200					205			
Glu	Gln	Val	Glu	Asp	Ala	Thr	Asn	Gly	Leu	Phe	Ser	Thr	Leu	Ser	Ser
	210					215					220				
Ser	Ala	Ile	Cys	Ser	Ser	Ala	Thr	Pro	Asp	Cys	Arg	Val	Glu	Ala	His
225					230					235					240
Pro	Cys	Glu	His	Arg	Thr	Leu	Glu	Met	Val	Arg	Glu	Phe	Ala	Gly	Asn
				245				250						255	
Ala	Pro	Cys	Trp	Arg	Gly	Ser	Arg	Arg	Thr	Leu	Ala	Val	Leu	Ala	Ala
			260					265					270		
His	Cys	Pro	Phe	Tyr	Ser	Trp	Lys	Arg	Val	Phe	Leu	Thr	His	Pro	Ala
		275					280					285			
Thr	Cys	Tyr	Arg	Thr	Thr	Cys	Pro	Gly	Pro	Cys	Asp	Ser	Gln	Pro	Cys
	290					295					300				
Gln	Asn	Gly	Gly	Thr	Cys	Val	Pro	Glu	Gly	Leu	Asp	Gly	Tyr	Gln	Cys
305					310					315					320
Leu	Cys	Pro	Leu	Ala	Phe	Gly	Gly	Glu	Ala	Asn	Cys	Ala	Leu	Lys	Leu
				325					330					335	
Ser	Leu	Glu	Cys	Arg	Val	Asp	Leu	Leu	Phe	Leu	Leu	Asp	Ser	Ser	Ala
			340					345					350		
Gly	Thr	Thr	Leu	Asp	Gly	Phe	Leu	Arg	Ala	Lys	Val	Phe	Val	Lys	Arg
		355					360					365			
Phe	Val	Arg	Ala	Val	Leu	Ser	Glu	Asp	Ser	Arg	Ala	Arg	Val	Gly	Val
	370					375					380				
Ala	Thr	Tyr	Ser	Arg	Glu	Leu	Leu	Val	Ala	Val	Pro	Val	Gly	Glu	Tyr
385					390					395					400
Gln	Asp	Val	Pro	Asp	Leu	Val	Trp	Ser	Leu	Asp	Gly	Ile	Pro	Phe	Arg
				405					410					415	
Gly	Gly	Pro	Thr	Leu	Thr	Gly	Ser	Ala	Leu	Arg	Gln	Ala	Ala	Glu	Arg
			420					425					430		
Gly	Phe	Gly	Ser	Ala	Thr	Arg	Thr	Gly	Gln	Asp	Arg	Pro	Arg	Arg	Val
	435						440					445			
Val	Val	Leu	Leu	Thr	Glu	Ser	His	Ser	Glu	Asp	Glu	Val	Ala	Gly	Pro
	450					455					460				
Ala	Arg	His	Ala	Arg	Ala	Arg	Glu	Leu	Leu	Leu	Gly	Val	Gly	Ser	
465					470					475					480
Glu	Ala														

Ser	Ala	Gly	Thr	Ala	Leu	Leu	His	Ile	Tyr	Asp	Lys	Val	Met	Thr	Val
610						615					620				
Gln	Arg	Gly	Ala	Arg	Pro	Gly	Val	Pro	Lys	Ala	Val	Val	Val	Leu	Thr
625					630					635					640
Gly	Gly	Arg	Gly	Ala	Glu	Asp	Ala	Ala	Val	Pro	Ala	Gln	Lys	Leu	Arg
				645						650				655	
Asn	Asn	Gly	Ile	Ser	Val	Leu	Val	Val	Gly	Val	Gly	Pro	Val	Leu	Ser
			660						665				670		
Glu	Gly	Leu	Arg	Arg	Leu	Ala	Gly	Pro	Arg	Asp	Ser	Leu	Ile	His	Val
		675					680					685			
Ala	Ala	Tyr	Ala	Asp	Ileu	Arg	Tyr	His	Gln	Asp	Val	Leu	Ile	Glu	Trp
	690					695					700				
Leu	Cys	Gly	Glu	Ala	Lys	Gln	Pro	Val	Asn	Leu	Cys	Lys	Pro	Ser	Pro
705					710					715					720
Cys	Met	Asn	Glu	Gly	Ser	Cys	Val	Leu	Gln	Asn	Gly	Ser	Tyr	Arg	Cys
				725					730					735	
Lys	Cys	Arg	Asp	Gly	Trp	Glu	Gly	Pro	His	Cys	Glu	Asn	Arg	Glu	Trp
			740					745					750		
Ser	Ser	Cys	Ser	Val	Cys	Val	Ser	Gln	Gly	Trp	Ile	Leu	Glu	Thr	Pro
		755					760					765			
Leu	Arg	His	Met	Ala	Pro	Val	Gln	Glu	Gly	Ser	Ser	Arg	Thr	Pro	Pro
	770					775					780				
Ser	Asn	Tyr	Arg	Glu	Gly	Leu	Gly	Thr	Glu	Met	Val	Pro	Thr	Phe	Trp
785					790					795					800
Asn	Val	Cys	Ala	Pro	Gly	Pro									
					805										

<210> 3

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: conserved  
cytokine receptor extracellular motif

<220>

<221> MOD\_RES

<222> (3)

<223> Xaa = any amino acid

<400> 3

Trp Ser Xaa Trp Ser

1

5